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| EXAMINER | |
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| WHALEY, PABLO S | |

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**Please find below and/or attached an Office communication concerning this application or proceeding.**

The time period for reply, if any, is set in the attached communication.

| Office Action Summary | Application No. | Applicant(s) | |
|---|---|---|---|
| | 10/644,594 | FRUDAKIS ET AL. | |
| | Examiner | Art Unit | |
| | PABLO WHALEY | 1631 | |

*-- The MAILING DATE of this communication appears on the cover sheet with the correspondence address --*

**Period for Reply**

A SHORTENED STATUTORY PERIOD FOR REPLY IS SET TO EXPIRE 3 MONTH(S) OR THIRTY (30) DAYS, WHICHEVER IS LONGER, FROM THE MAILING DATE OF THIS COMMUNICATION.

- Extensions of time may be available under the provisions of 37 CFR 1.136(a). In no event, however, may a reply be timely filed after SIX (6) MONTHS from the mailing date of this communication.
- If NO period for reply is specified above, the maximum statutory period will apply and will expire SIX (6) MONTHS from the mailing date of this communication.
- Failure to reply within the set or extended period for reply will, by statute, cause the application to become ABANDONED (35 U.S.C. § 133). Any reply received by the Office later than three months after the mailing date of this communication, even if timely filed, may reduce any earned patent term adjustment. See 37 CFR 1.704(b).

**Status**

1)☒ Responsive to communication(s) filed on *08/19/2008*.

2a)☒ This action is **FINAL**. 2b)☐ This action is non-final.

3)☐ Since this application is in condition for allowance except for formal matters, prosecution as to the merits is closed in accordance with the practice under *Ex parte Quayle*, 1935 C.D. 11, 453 O.G. 213.

**Disposition of Claims**

4)☒ Claim(s) *1 and 83-115* is/are pending in the application.

4a) Of the above claim(s) _____ is/are withdrawn from consideration.

5)☐ Claim(s) _____ is/are allowed.

6)☒ Claim(s) *1 and 83-115* is/are rejected.

7)☐ Claim(s) _____ is/are objected to.

8)☐ Claim(s) _____ are subject to restriction and/or election requirement.

**Application Papers**

9)☐ The specification is objected to by the Examiner.

10)☐ The drawing(s) filed on _____ is/are: a)☐ accepted or b)☐ objected to by the Examiner.

Applicant may not request that any objection to the drawing(s) be held in abeyance. See 37 CFR 1.85(a).

Replacement drawing sheet(s) including the correction is required if the drawing(s) is objected to. See 37 CFR 1.121(d).

11)☐ The oath or declaration is objected to by the Examiner. Note the attached Office Action or form PTO-152.

**Priority under 35 U.S.C. § 119**

12)☐ Acknowledgment is made of a claim for foreign priority under 35 U.S.C. § 119(a)-(d) or (f).

a)☐ All b)☐ Some * c)☐ None of:

1.☐ Certified copies of the priority documents have been received.

2.☐ Certified copies of the priority documents have been received in Application No. _____.

3.☐ Copies of the certified copies of the priority documents have been received in this National Stage application from the International Bureau (PCT Rule 17.2(a)).

* See the attached detailed Office action for a list of the certified copies not received.

**Attachment(s)**

1) ☒ Notice of References Cited (PTO-892)
2) ☐ Notice of Draftsperson's Patent Drawing Review (PTO-948)
3) ☐ Information Disclosure Statement(s) (PTO/SB/08) Paper No(s)/Mail Date _____.
4) ☐ Interview Summary (PTO-413) Paper No(s)/Mail Date. _____.
5) ☐ Notice of Informal Patent Application
6) ☐ Other: _____.

## DETAILED ACTION

### *Status of the Claims*

Claims 1 and 83-115 pending.

Claims 1 and 83-115 are rejected.

Claims 2-82 are cancelled.

### *Priority*

This application has been granted the benefit of priority to US Provisional Application 60/404,357, filed 8/19/2002.

### *Withdrawn Rejections*

The rejection of claims 1 and 83-115 under 35 U.S.C. 101 for non-statutory subject matter is withdrawn in view of applicant's amendments filed 08/19/2008.

### *Claim rejections - 35 USC § 112, 1st Paragraph*

Claims 1 and 83-115 are rejected under 35 U.S.C. 112, first paragraph, as failing to comply with the written description requirement. The claims contains subject matter which was not described in the specification in such a way as to reasonably convey to one skilled in the relevant art that the inventor, at the time the application was filed, had possession of the claimed invention.

**This is a NEW MATTER rejection.**

Claim 1 (step c) now recites the limitation "autosomal SNP." A review of the specification shows support for autosomal markers [p.47] and autosomal chromosomes [0235]. However no support has been found support "autosomal SNP" in the specification, and this limitation is not present within the scope of the original claims as filed. As the newly recited limitations are not supported by the originally filed claims or disclosure, the claims are rejected for reciting new matter. This rejection is necessitated by amendment.

***Claim Rejections - 35 USC § 112, 2nd Paragraph***

The following is a quotation of the second paragraph of 35 U.S.C. 112:

> The specification shall conclude with one or more claims particularly pointing out and distinctly claiming the subject matter which the applicant regards as his invention.

Claims 1 and 83-115 are rejected under 35 U.S.C. 112, second paragraph, as being indefinite for failing to particularly point out and distinctly claim the subject matter which applicant regards as the invention.

Claim 1 recites the phrase "gene encoding region." It is unclear as to the metes and bounds of said "gene encoding region" because it is not clear if the claimed subject matter excludes SNPs that are within a promoter region or an intron.

***Response to Arguments***

Applicant's arguments, filed 08/19/2008, that the phrase "gene encoding region" is an art recognized term that means a nucleic acid sequence which produces a product (as supported by Wikipedia) has been fully considered. Applicant's assertion that the claimed "gene encoding region" does not contain promoters or introns has also been fully considered.

In response, the Oxford English Dictionary (Copyright © Oxford University Press 2008) provides the following definition for the term "gene": "**1.** *Biol.* **a.** The basic unit of heredity in living organisms, originally recognized as a discrete physical factor associated with the inheritance of a particular morphological or physiological trait, and later shown to be located at a specific site on a chromosome and to consist of a sequence of DNA (or RNA in certain viruses) containing a code for a protein or RNA molecule, together with any associated sequences necessary for transcription and translation." Therefore the term "gene" has an art recognized definition that is different from the meaning argued by applicant, who asserts that genes do not contain promoter regions (i.e. regions for transcription and translation). Furthermore, Wikipedia is not an acceptable source of a definition because this is not a peer-reviewed publication and its authorship is unknown.

For the above reasons, it remains unclear as to the metes and bounds of said "gene encoding region" because it is unclear whether the claimed gene encoding region excludes SNPs that are within a promoter region or an intron. This rejection is maintained.

***Claim Rejections - 35 USC § 103***

The following is a quotation of 35 U.S.C. 103(a) which forms the basis for all obviousness rejections set forth in this Office action:

> (a) A patent may not be obtained though the invention is not identically disclosed or described as set forth in section 102 of this title, if the differences between the subject matter sought to be patented and the prior art are such that the subject matter as a whole would have been obvious at the time the invention was made to a person having ordinary skill in the art to which said subject

matter pertains. Patentability shall not be negatived by the manner in which the invention was made.

This application currently names joint inventors. In considering patentability of the claims under 35 U.S.C. 103(a), the examiner presumes that the subject matter of the various claims was commonly owned at the time any inventions covered therein were made absent any evidence to the contrary. Applicant is advised of the obligation under 37 CFR 1.56 to point out the inventor and invention dates of each claim that was not commonly owned at the time a later invention was made in order for the examiner to consider the applicability of 35 U.S.C. 103(c) and potential 35 U.S.C. 102(e), (f) or (g) prior art under 35 U.S.C. 103(a).

Claims 1, 83-86, 90-101, and 104-109 are rejected under 35 U.S.C. 103(a) as being unpatentable over Parra et al. (Am. J. Physical Antropol., January 2001, Vol. 114, Issue 1, p. 18-29), in view of Shriver et al. (American Journal of Human Genetics, 1997, Vol. 60, p.957-964) in the IDS filed 5/20/2004, in view of Kaessmann et al. (Nature Genetics, May 1999, Vol. 22, p.78-81), and in view of Vines (New Scientist, 1995, Vol. 147, No. 1985, p.34-42).

Applicant's amendments, filed 08/19/2008, have amended claim 1 to recite a step for generating a second population of SNPs containing an autosomal SNP, and wherein at least one SNP of the second population of SNPs is not located within a gene encoding region, as in claim 1 (step c).

Parra teaches a method for inferring ancestral proportions and admixture in six different populations from different regions [See Abstract]. Parent populations and non-parental populations are disclosed [p.19, Subjects and Methods]. Parra identifies a population of ten SNP markers comprising and delta values > 0.4 between one or more populations [Table 1, last column]. Parent samples are contacted with markers using standard PCR genotyping for determining allele frequencies [See p.20, Col. 1 and Table 1, last column]. A combination of SNP markers are selected to obtain an estimate of admixture for a sub-population [p.21, Col. 1, ¶ 2, and Fig. 1], wherein allele frequencies of the SNP markers are > 1% [Table 1], which is a teaching for minor allele frequencies. Parra shows the use of markers that are

unlinked to certain loci [p.20, Col. 1, and p.23, Col. 2]. Parra calculates the frequency differences between populations based on SNPs [p.23, Col. 2]. The population structure is then determined using a predetermined confidence interval and infers the proportional ancestry of the non-parental population [p. 21 and Table 2]. Parra also shows fitting genotype frequencies to Hardy-Weinberg proportions and suggest the selection of genetic markers that show homogeneity with Africa and Europe based on allele frequency [p.20, Statistical Analysis]. Additionally, Parra shows two-way and three-way comparison of populations that are both intracontinental and intercontinental [Table 1, Fig. 1, and p. 22], with delta values > 0.4. Parra discloses a biogeographical ancestry trait (BGA) [Fig. 1], and admixture proportions of samples estimated using maximum likelihood calculations [p.20, Col. 2, ¶2 and ¶3]. Parra shows proportional ancestry comprising a three-way comparison of sub-populations of African-Americans and the distribution percentage of European alleles within this sub-population [Fig. 1] derived from maximum-likelihood methods [p.25, Col. 2]. Parra shows SNPs detected in a subpopulation of non-parental individuals for determining sub-population structure [Fig. 1]. Regarding "autosomal SNP", Parra teaches selecting a population of single nucleotide polymorphisms (SNPs) and combining these markers to estimate admixture [p.19-20, DNA Analysis]. In this population of markers, at least one is an autosomal polymorphism marker (D11S429) [p.20, Col. 1, and Table 1] that is associated with ancestry [Table 5], which shows the use at least one autosomal SNP that may be correlated but not linked to a gene-trait.

Parra does not teach generating a second population of SNPs wherein the second population is an autosomal SNP, and wherein at least one SNP of the second population of SNPs is not located within a gene encoding region, as in claim 1 (step c).

Parra does not specifically teach performing a likelihood determination for affiliation with an East Asian ancestral group as required by claims 98, or four-way comparisons as in claim 101.

Kaessmann teaches the use of non-coding region DNA for determining point mutations (i.e. SNPs) and polymorphic positions to gain insight to human ancestry [p.78, Col. 1 and 2, and Fig. 2]. A class of nuclear loci that is useful for evolutionary analysis is also disclosed [p.80, Col. 2]. Kaessmann also shows a map of the world indicating approximate origins of individuals studied [Fig. 1]. Kaessman also shows that the use of non-coding DNA in inheritance applications is advantageous because it is highly unlikely to be the direct target of positive or negative selection [p.79, Col. 1].

Shriver teaches a method for identifying a set of genetic markers using likelihood analysis that allows the confident determination of ethnicity for use in a forensic setting [Abstract and p.964, Discussion]. In particular, Shriver presents population specific alleles (PSAs) [p.957, Col. 2], as well as methods for calculating allele-frequency differentials between test samples of different populations [p.958, Col. 2] and for calculating likelihood values for different loci [Table 1, and Table 2 ]. Shriver does not specifically teach "four-way" comparison. However, Shriver performs two-way and three-way comparisons between multiple populations [Fig. 1-4]. Therefore, it would be obvious to one of ordinary skill in the art to perform a four-way comparison among four ancestral groups, as in claim 101. Shriver also suggests similar markers could be developed for the identification of other populations including those of Asian origin [p.963, last ¶, Col. 1].

Vines teaches neutral non-coding polymorphism markers (i.e. junk DNA) that are beneficially used as signposts for disease and potential markers for racial origins [p.36, Col. 3]. Vines teaches that a vast majority of genetic variations occur in the "neutral" non-coding regions of genes [p.36, Col. 2], and suggests that genetic analysis using non-coding region markers will produce new correlations that bolster racial classification and forensic science [p.36, Col. 2].

It would have been obvious to one of ordinary skill in the art at the time of the instant invention to modify the method of Parra by selecting a second set of SNPs that hybridize to a sample nucleic acid to generate a second population of SNPs containing an autosomal SNP, and wherein at least one SNP of the

second population of SNPs is not located within a gene encoding region, as in claim 1 (step c), since Parra shows selecting a first population of SNP markers that includes at least one autosomal polymorphism marker (D11S429) and further combining these markers (i.e. a second population) to estimate admixture [p.19-20, DNA Analysis, Table 1]. The motivation would have been to select the most informative SNP markers available for admixture (high frequency difference) between populations to avoid [p.19-20, DNA Analysis, p.20, Col. 2, ¶1].

It would have been obvious to one of ordinary skill in the art at the time of the instant invention to modify the method of Parra by selecting at least one SNP that is not located within a gene encoding region, as in claim 1 (step c), since Kaessmann uses non-coding region DNA for determining point mutations (i.e. SNPs) and polymorphic positions to gain insight to human ancestry [p.78, Col. 1 and 2, and Fig. 2]. The motivation would have been to improve ancestral prediction by using markers that are highly unlikely to be the direct target of positive or negative selection, as suggested by Kaessmann [p.79, Col. 1]. Additional motivation for using non-coding region markers is provided by Vines, who shows that non-coding polymorphic sequences are beneficial as potential markers for racial origins [p.36, Col. 3] since a vast majority of genetic variations occur in the "neutral" non-coding regions of genes [p.36, Col. 2].

It would further have been obvious to one of ordinary skill in the art at the time of the instant invention to modify the method of Parra by performing a likelihood determination for affiliation with an East Asian ancestral group as required by claims 98, since Shriver identifies genetic markers using likelihood analysis [Abstract and p.964, Discussion, Table 1, and Table 2] and suggests markers for those of Asian ancestry [p.963, last ¶, Col. 1]. The motivation would have been to allow for the confident determination of ethnicity in forensic settings, as suggested by Shriver [Abstract and p.964, Discussion, Table 1, and Table 2].

It would further have been obvious to one of ordinary skill in the art at the time of the instant invention to modify the method of Parra by performing four-way comparisons, as in claim 101, since Shriver performs two-way and three-way comparisons between multiple populations [Fig. 1-4]. The motivation would have been to identify other populations that share common ancestry, as suggested by Shriver [p.963, Col. 1, last ¶, and Col. 2].

Claims 87-89 and 110-115 are rejected under 35 U.S.C. 103(a) as being unpatentable over Parra et al. (Am. J. Physical Antropol., January 2001, Vol. 114, Issue 1, p. 18-29), in view of Shriver et al. (American Journal of Human Genetics, 1997, Vol. 60, p.957-964), in view of Kaessmann et al. (Nature Genetics, May 1999, Vol. 22, p.78-81), and in view of Vines (New Scientist, 1995, Vol. 147, No. 1985, p.34-42), as applied to claims 1, 83-86, 90-101, and 104-109 above, and further in view of Sorenson et al. (US 2003/0172065; Filed Mar. 29, 2002).

Parra, Shriver, Kaessmann, and Vines make obvious a method for inferring ancestral proportions and admixture, as set forth above.

Parra, Shriver, Kaessmann, and Vines do not specifically teach contacting samples with high numbers of SNPs as in claims 87- 89.

Parra, Shriver, Kaessmann, and Vines do not specifically teach proportional ancestries comprising a photo of a person from whom the known proportional ancestry was determined, as in claims 110-115.

Sorenson discloses a genealogical research and record keeping system for identifying commonalities in haplotypes from biological samples [Abstract]. In particular, Sorenson teaches thousands of known genetic markers and millions of characterized SNPs may be analyzed [0042], [Fig. 4] for identifying a population structure [0032], [0046]-[0047] that correlates with markers and a trait, as in

claim 87-89. Sorenson also discloses prior art genetic records of human eye, hair and skin color, height and other physical characteristics [0009], and ancestral data stored on microfiche and on a number of other electronic media formats including the internet [0003], which is broadly interpreted as a teaching for digital information and pictures as in claims 110-115.

It would have been obvious to one of ordinary skill in the art at the time of the instant invention to modify the method made obvious by Parra, Shriver, Kaessmann, and Vines by contacting samples with high numbers of SNPs as in claims 87- 89, since Sorenson teaches genetic analysis using thousands of known genetic markers and millions of characterized SNPs [0042, Fig. 4]. The motivation would have been to identify a population structure that correlates with markers and a trait, as suggested by Sorenson [0032, 0046-0047] or identify previously unknown biological relationships by correlating genetic information with genealogical information [Sorenson, 0015].

It would further have been obvious to one of ordinary skill in the art at the time of the instant invention to modify the method made obvious by Parra, Shriver, Kaessmann, and Vines by using proportional ancestries comprising a photo of a person from whom the known proportional ancestry was determined, as in claims 110-115, since Sorenson teaches genetic records and ancestral data stored on microfiche and in electronic media format [0003, 0009]. The motivation would have been to improve the sharing of ancestral data using electronic formats that are suitable for the internet, as suggested by Sorenson [0003].

Claims 102 and 103 are rejected under 35 U.S.C. 103(a) as being unpatentable over Parra et al. (Am. J. Physical Antropol., January 2001, Vol. 114, Issue 1, p. 18-29), in view of Shriver et al. (American Journal of Human Genetics, 1997, Vol. 60, p.957-964), in view of Kaessmann et al. (Nature Genetics, May 1999, Vol. 22, p.78-81), and in view of Vines (New Scientist, 1995, Vol. 147, No. 1985, p.34-42), as applied to

claims 1, 83-86, 90-101, and 104-109 above, and in further view of Pritchard et al. (Theoretical Population Biology, 2001, Vol. 60, p. 227-237).

Parra, Shriver, Kaessmann, and Vines make obvious a method for inferring ancestral proportions and admixture, as set forth above.

Parra, Shriver, Kaessmann, and Vines do not teach generating a graphical representation, as in claims 102 and 103.

Pritchard teaches methods for inferring proportional ancestry of different ancestral groups, and graphically displaying ancestral results in triangular format [Fig. 1], as in claims 102 and 103. Pritchard also teaches a computer-based program STRUCTURE for estimating population structure for 20 data sets of 50, 200, and 1000 biallelic markers [p. 232, Results].

It would have been obvious to one of ordinary skill in the art at the time of the instant invention to practice the method made obvious by Parra, Shriver, Kaessmann, and Vines by generating a graphical representation, as in claims 102 and 103, since Pritchard shows graphically displaying ancestral results in triangular format [Fig. 1]. The motivation would have been to use a user-friendly graphical method for inferring ancestry in a plurality of populations, as suggested by Pritchard [Fig. 1].

***Response to Arguments***

Applicant's arguments, filed 08/19/2008, that none of the cited references describes a second population of SNPs as in claim 1, step c), where the SNP may be correlated with but not linked to a gene-linked trait, wherein the second population of SNPs is an autosomal SNP, and wherein the at least one SNP of the second population of SNPs is not located within a gene encoding region. In response,

regarding "autosomal SNP", Parra teaches selecting a population of single nucleotide polymorphisms (SNPs) and combining these markers to estimate admixture [p.19-20, DNA Analysis]. In this population of markers, at least one is an autosomal polymorphism marker (D11S429) [p.20, Col. 1, and Table 1], which shows the use at least one autosomal SNP. Parra does not teach selecting SNPs that hybridize to a sample nucleic acid to generate a second population of SNPs containing an autosomal SNP, and wherein at least one SNP of the second population of SNPs is not located within a gene encoding region, as in claim 1 (step c). Kaessmann teaches the use of non-coding region DNA for determining point mutations (i.e. SNPs) and polymorphic positions to gain insight to human ancestry [p.78, Col. 1 and 2, and Fig. 2]. A class of nuclear loci that is useful for evolutionary analysis is also disclosed [p.80, Col. 2]. Kaessmann also shows a map of the world indicating approximate origins of individuals studied [Fig. 1]. Kaessman also shows that the use of non-coding DNA in inheritance applications is advantageous because it is highly unlikely to be the direct target of positive or negative selection [p.79, Col. 1].

In response to applicant's arguments that there is no suggestion or motivation to combine the above references with a reasonable expectation of success, it would have been obvious to one of ordinary skill in the art at the time of the instant invention to modify the method of Parra by selecting a second set of SNPs that hybridize to a sample nucleic acid to generate a second population of SNPs containing an autosomal SNP, and wherein at least one SNP of the second population of SNPs is not located within a gene encoding region, as in claim 1 (step c), since Parra shows selecting a first population of SNP markers that includes at least one autosomal polymorphism marker (D11S429) and further combining these markers (i.e. a second population) to estimate admixture [p.19-20, DNA Analysis, Table 1]. The motivation would have been to select the most informative SNP markers available for admixture (high frequency difference) between populations to avoid [p.19-20, DNA Analysis, p.20, Col. 2, ¶1]. It would further have been obvious to one of ordinary skill in the art at the time of the instant invention to modify the method of Parra by selecting at least one SNP that is not located within a gene encoding region, as in

claim 1 (step c), since Kaessmann uses non-coding region DNA for determining point mutations (i.e. SNPs) and polymorphic positions to gain insight to human ancestry [p.78, Col. 1 and 2, and Fig. 2]. The motivation would have been to improve ancestral prediction by using markers that are highly unlikely to be the direct target of positive or negative selection, as suggested by Kaessmann [p.79, Col. 1]. Additional motivation for using non-coding region markers is provided by Vines, who shows that non-coding polymorphic sequences are beneficial as potential markers for racial origins [p.36, Col. 3] since a vast majority of genetic variations between populations occur in the "neutral" non-coding regions of genes [p.36, Col. 2].

In response to applicant's arguments that there is no suggestion or motivation to combine the teachings of Parra, Shriver, Kaessmann, Vines, and Sorenson with a reasonable expectation of success, it would have been obvious to one of ordinary skill in the art at the time of the instant invention to modify the method made obvious by Parra, Shriver, Kaessmann, and Vines by contacting samples with high numbers of SNPs as in claims 87- 89, since Sorenson teaches genetic analysis using thousands of known genetic markers and millions of characterized SNPs [0042, Fig. 4]. The motivation would have been to identify a population structure that correlates with markers and a trait, as suggested by Sorenson [0032, 0046-0047] or identify previously unknown biological relationships by correlating genetic information with genealogical information [Sorenson, 0015]. It would further have been obvious to one of ordinary skill in the art at the time of the instant invention to modify the method made obvious by Parra, Shriver, Kaessmann, and Vines by using proportional ancestries comprising a photo of a person from whom the known proportional ancestry was determined, as in claims 110-115, since Sorenson teaches genetic records and ancestral data stored on microfiche and in electronic media format [0003, 0009]. The motivation would have been to improve the sharing of ancestral data using electronic formats that are suitable for the internet, as suggested by Sorenson [0003].

In response to applicant's arguments that there is no suggestion or motivation to combine the teachings of Parra, Shriver, Kaessmann, Vines, Sorenson, and Pritchard with a reasonable expectation of success, it would have been obvious to one of ordinary skill in the art at the time of the instant invention to practice the method made obvious by Parra, Shriver, Kaessmann, and Vines by generating a graphical representation, as in claims 102 and 103, since Pritchard shows graphically displaying ancestral results in triangular format [Fig. 1]. The motivation would have been to use a user-friendly graphical method for inferring ancestry in a plurality of populations, as suggested by Pritchard [Fig. 1].

In response to applicant's arguments that the cited references teach away from the claimed invention, it has been held that a prior art reference must either be in the field of applicant's endeavor or, if not, then be reasonably pertinent to the particular problem with which the applicant was concerned, in order to be relied upon as a basis for rejection of the claimed invention. See In re Oetiker, 977 F.2d 1443, 24 USPQ2d 1443 (Fed. Cir. 1992). In this case, the cited references are directed to the areas of population genetics, proportional ancestry, and admixture inference. Therefore, the cited references are relevant to the claimed subject matter. For the above reasons, these rejections are maintained.

***Conclusion***

Applicant's amendment necessitated the new ground(s) of rejection presented in this Office action. Accordingly, **THIS ACTION IS MADE FINAL**. See MPEP § 706.07(a). Applicant is reminded of the extension of time policy as set forth in 37 CFR 1.136(a).

A shortened statutory period for reply to this final action is set to expire THREE MONTHS from the mailing date of this action. In the event a first reply is filed within TWO MONTHS of the mailing date of this final action and the advisory action is not mailed until after the end of the THREE-MONTH shortened statutory period, then the shortened statutory period will expire on the date the advisory action

is mailed, and any extension fee pursuant to 37 CFR 1.136(a) will be calculated from the mailing date of the advisory action. In no event, however, will the statutory period for reply expire later than SIX MONTHS from the date of this final action.

Any inquiry concerning this communication or earlier communications from the examiner should be directed to Pablo Whaley whose telephone number is (571)272-4425. The examiner can normally be reached on 9:30am - 6pm.

If attempts to reach the examiner by telephone are unsuccessful, the examiner's supervisor, Marjorie Moran can be reached at 571-272-0720. The fax phone number for the organization where this application or proceeding is assigned is 571-273-8300.

Information regarding the status of an application may be obtained from the Patent Application Information Retrieval (PAIR) system. Status information for published applications may be obtained from either Private PAIR or Public PAIR. Status information for unpublished applications is available through Private PAIR only. For more information about the PAIR system, see http://pair-direct.uspto.gov. Should you have questions on access to the Private PAIR system, contact the Electronic Business Center (EBC) at 866-217-9197 (toll-free).

**/Pablo S. Whaley/**

Patent Examiner

Art Unit 1631

/John S. Brusca/
Primary Examiner, Art Unit 1631